

5-Fluorouracil–dimethyl sulfoxide (1/1)**Ashley T. Hulme*** and
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Received 1 September 2004
Accepted 8 September 2004
Online 18 September 2004

The title compound, $C_4H_3FN_2O_2 \cdot C_2H_6OS$, crystallizes in the monoclinic space group $P2_1/c$, with one molecule of 5-fluorouracil and one molecule of dimethyl sulfoxide (DMSO) in the asymmetric unit. The crystal structure contains hydrogen-bonded ribbons of alternating 5-fluorouracil and DMSO molecules which stack, forming non-interacting layers parallel to the (100) planes.

Comment

In the course of a polymorph screen performed on 5-fluorouracil three solvates were discovered; the crystal structure of one of these solvates is reported here. The title compound, (I), crystallizes in the space group $P2_1/c$ with one molecule of 5-fluorouracil and one molecule of dimethyl sulfoxide (DMSO) in the asymmetric unit.

Key indicators

Single-crystal X-ray study

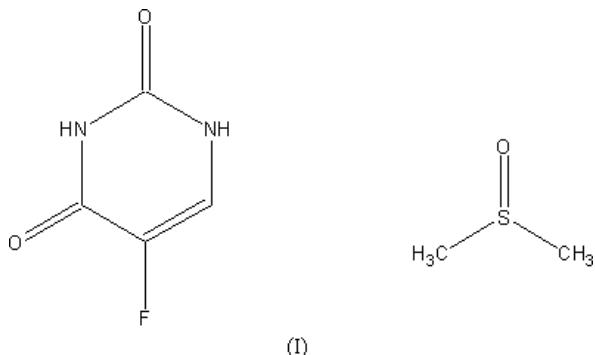
 $T = 150\text{ K}$ Mean $\sigma(C-C) = 0.002\text{ \AA}$

Disorder in main residue

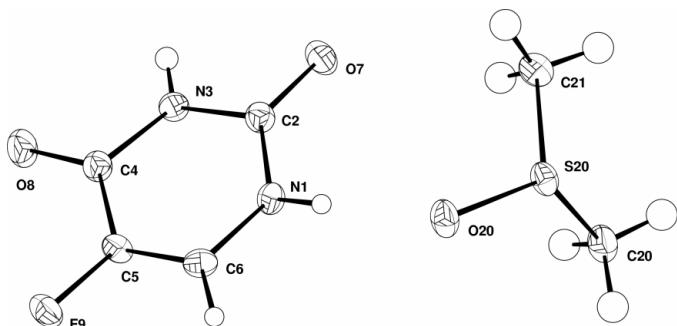
 R factor = 0.036 wR factor = 0.090

Data-to-parameter ratio = 15.2

For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.



The S atom in the DMSO molecule is disordered over two sites, with a 95:5 occupancy ratio. The minor site ($S20'$) exhibits the opposite pyrimidisation of the DMSO molecule, compared to the major site ($S20$). Fig. 1 shows the asymmetric unit, with only the major sulfur position shown.

**Figure 1**

View (Watkin *et al.*, 1996) of the asymmetric unit of the title compound, with 50% probability displacement ellipsoids. H atoms are drawn as spheres of arbitrary radii.

Two conventional hydrogen bonds, of the type N—H···O, occur in the structure. The O atom of the DMSO molecule acts as a hydrogen-bond acceptor for two symmetry-related 5-fluorouracil molecules (Table 1).

The crystal structure contains hydrogen-bonded ribbons of alternating 5-fluorouracil and DMSO molecules (Fig. 2). These ribbons stack, forming form non-interacting layers parallel to the (100) planes.

Experimental

5-Fluorouracil was obtained from the Aldrich Chemical Company Inc. The crystals of the title compound were grown by vapour diffusion of diethyl ether into a saturated solution of 5-fluorouracil in DMSO.

Crystal data



$M_r = 208.21$

Monoclinic, $P2_1/c$

$a = 9.8831 (10) \text{ \AA}$

$b = 10.8128 (11) \text{ \AA}$

$c = 8.6842 (9) \text{ \AA}$

$\beta = 107.397 (2)^\circ$

$V = 885.58 (16) \text{ \AA}^3$

$Z = 4$

$D_x = 1.562 \text{ Mg m}^{-3}$

Mo $K\alpha$ radiation

Cell parameters from 3031 reflections

$\theta = 2.9\text{--}28.0^\circ$

$\mu = 0.36 \text{ mm}^{-1}$

$T = 150 (2) \text{ K}$

Block, colourless

$0.29 \times 0.21 \times 0.11 \text{ mm}$

Data collection

Bruker SMART APEX diffractometer

Narrow-frame ω scans

Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996)

$T_{\min} = 0.903$, $T_{\max} = 0.962$

7672 measured reflections

2128 independent reflections

1922 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.022$

$\theta_{\max} = 28.3^\circ$

$h = -13 \rightarrow 12$

$k = -14 \rightarrow 14$

$l = -11 \rightarrow 11$

Refinement

Refinement on F^2

$R[F^2 > 2\sigma(F^2)] = 0.036$

$wR(F^2) = 0.090$

$S = 1.07$

2127 reflections

140 parameters

H atoms treated by a mixture of independent and constrained refinement

$$w = 1/[\sigma^2(F_o^2) + (0.0401P)^2 + 0.5099P]$$

where $P = (F_o^2 + 2F_c^2)/3$

$(\Delta/\sigma)_{\max} < 0.001$

$\Delta\rho_{\max} = 0.40 \text{ e \AA}^{-3}$

$\Delta\rho_{\min} = -0.54 \text{ e \AA}^{-3}$

Table 1

Hydrogen-bonding geometry (\AA , $^\circ$).

$D-\text{H}\cdots A$	$D-\text{H}$	$\text{H}\cdots A$	$D\cdots A$	$D-\text{H}\cdots A$
N1—H1···O20	0.79 (2)	2.04 (2)	2.838 (2)	175 (2)
N3—H3···O20 ⁱ	0.82 (2)	1.97 (2)	2.790 (2)	173 (2)
N1—H1···S20 ⁱ	0.79 (2)	2.56 (2)	3.266 (8)	149 (2)
N3—H3···S20 ⁱ	0.82 (2)	2.89 (2)	3.666 (1)	157 (2)

Symmetry code: (i) $1 - x, \frac{1}{2} + y, \frac{1}{2} - z$.

The S atom in the DMSO molecule is disordered over two sites and was modelled anisotropically, with site occupancy 95:5. The S—O and S—C distances in the major and minor components were restrained to be equal within $\pm 0.01 \text{ \AA}$. All H atoms on 5-fluorouracil were located in a difference map and were refined isotropically; N—H = 0.79 (2) and 0.82 (2) \AA , and C—H = 0.94 (2) \AA . The H-atom positions on the methyl group were idealized and refined using a riding model [C—H = 0.96 \AA and $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$].

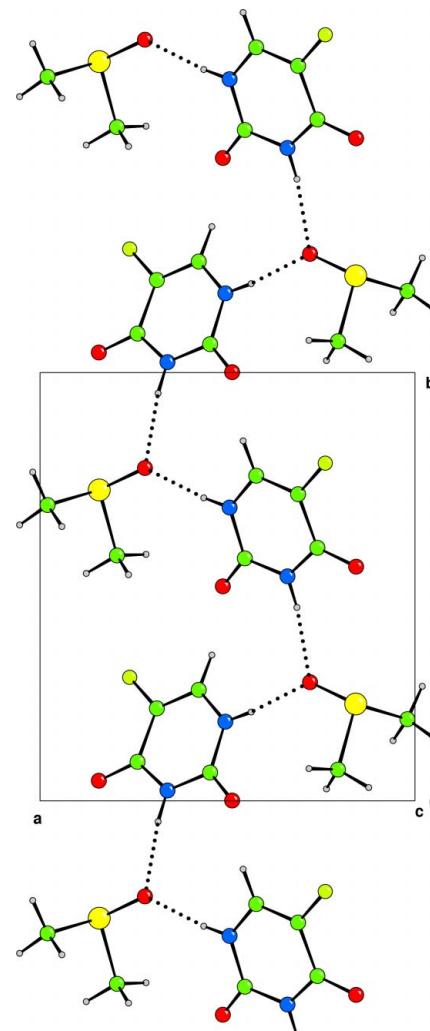


Figure 2

Hydrogen-bonded ribbon motif, made up of alternating 5-fluorouracil and DMSO molecules. Hydrogen bonds are shown as dashed lines.

Data collection: *SMART* (Bruker, 1998); cell refinement: *SAINT* (Bruker, 1998); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *CAMERON* (Watkin *et al.*, 1996); software used to prepare material for publication: *SHELXL97*.

The authors acknowledge the Research Councils UK Basic Technology Programme for supporting ‘Control and Prediction of the Organic Solid State’.

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supporting information

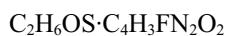
Acta Cryst. (2004). E60, o1786–o1787 [https://doi.org/10.1107/S1600536804022275]

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Hall symbol: -P 2ybc

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$V = 885.58 (16) \text{ \AA}^3$

$Z = 4$

$F(000) = 432$

$D_x = 1.562 \text{ Mg m}^{-3}$

Mo $K\alpha$ radiation, $\lambda = 0.71073 \text{ \AA}$

Cell parameters from 3031 reflections

$\theta = 2.9\text{--}28.0^\circ$

$\mu = 0.36 \text{ mm}^{-1}$

$T = 150 \text{ K}$

Block, colourless

$0.29 \times 0.21 \times 0.11 \text{ mm}$

Data collection

Bruker SMART APEX
diffractometer

Radiation source: sealed tube

Graphite monochromator

ω rotation with narrow frames scans

Absorption correction: multi-scan
(SADABS; Sheldrick, 1996)

$T_{\min} = 0.903$, $T_{\max} = 0.962$

7672 measured reflections

2128 independent reflections

1922 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.022$

$\theta_{\max} = 28.3^\circ$, $\theta_{\min} = 2.2^\circ$

$h = -13 \rightarrow 12$

$k = -14 \rightarrow 14$

$l = -11 \rightarrow 11$

Refinement

Refinement on F^2

Least-squares matrix: full

$R[F^2 > 2\sigma(F^2)] = 0.036$

$wR(F^2) = 0.090$

$S = 1.07$

2127 reflections

140 parameters

7 restraints

Primary atom site location: structure-invariant
direct methods

Secondary atom site location: found from delta

F

Hydrogen site location: found from delta F

H atoms treated by a mixture of independent

and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0401P)^2 + 0.5099P]$

where $P = (F_o^2 + 2F_c^2)/3$

$(\Delta/\sigma)_{\max} < 0.001$

$\Delta\rho_{\max} = 0.40 \text{ e \AA}^{-3}$

$\Delta\rho_{\min} = -0.54 \text{ e \AA}^{-3}$

Special details

Experimental. The sulfur atom in the DMSO molecule is disordered and is modelled anisotropically, with site occupancy 95:5.

Geometry. All e.s.d.'s (except the e.s.d. in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell e.s.d.'s are taken into account individually in the estimation of e.s.d.'s in distances, angles and torsion angles; correlations between e.s.d.'s in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell e.s.d.'s is used for estimating e.s.d.'s involving l.s. planes.

Refinement. Refinement of F^2 against ALL reflections. The weighted R -factor wR and goodness of fit S are based on F^2 , conventional R -factors R are based on F , with F set to zero for negative F^2 . The threshold expression of $F^2 > \sigma(F^2)$ is used only for calculating R -factors(gt) etc. and is not relevant to the choice of reflections for refinement. R -factors based on F^2 are statistically about twice as large as those based on F , and R -factors based on ALL data will be even larger.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (\AA^2)

	<i>x</i>	<i>y</i>	<i>z</i>	$U_{\text{iso}}^*/U_{\text{eq}}$	Occ. (<1)
S20	0.15779 (4)	0.27388 (4)	-0.05029 (5)	0.01947 (14)	0.9452 (19)
S20'	0.1956 (8)	0.3387 (7)	0.0775 (10)	0.047 (3)	0.0548 (19)
O20	0.27984 (12)	0.22286 (10)	0.08812 (14)	0.0242 (3)	
C20	0.02017 (18)	0.30934 (19)	0.0348 (2)	0.0310 (4)	
H20A	-0.0187	0.2340	0.0621	0.047*	0.9452 (19)
H20B	-0.0530	0.3549	-0.0420	0.047*	0.9452 (19)
H20C	0.0576	0.3583	0.1303	0.047*	0.9452 (19)
H20D	0.0033	0.2592	0.1184	0.047*	0.0548 (19)
H20E	-0.0138	0.2671	-0.0667	0.047*	0.0548 (19)
H20F	-0.0289	0.3867	0.0289	0.047*	0.0548 (19)
C21	0.20530 (19)	0.42683 (17)	-0.0857 (2)	0.0296 (4)	
H21A	0.2812	0.4246	-0.1335	0.044*	0.9452 (19)
H21B	0.2356	0.4710	0.0147	0.044*	0.9452 (19)
H21C	0.1249	0.4678	-0.1576	0.044*	0.9452 (19)
H21D	0.3041	0.4445	-0.0672	0.044*	0.0548 (19)
H21E	0.1541	0.5029	-0.0904	0.044*	0.0548 (19)
H21F	0.1691	0.3833	-0.1860	0.044*	0.0548 (19)
C6	0.57652 (17)	0.24074 (15)	0.4738 (2)	0.0203 (3)	
F9	0.76106 (11)	0.21144 (9)	0.71240 (12)	0.0274 (2)	
O7	0.48751 (13)	0.49901 (12)	0.21670 (14)	0.0288 (3)	
O8	0.84328 (13)	0.45295 (12)	0.68615 (15)	0.0300 (3)	
N1	0.50578 (15)	0.31511 (13)	0.34764 (17)	0.0202 (3)	
N3	0.66006 (14)	0.47552 (13)	0.45536 (16)	0.0195 (3)	
C2	0.54651 (16)	0.43374 (15)	0.33165 (18)	0.0194 (3)	
C4	0.73994 (16)	0.40891 (15)	0.58632 (19)	0.0197 (3)	
C5	0.68843 (17)	0.28387 (14)	0.58802 (19)	0.0199 (3)	
H1	0.439 (2)	0.2926 (18)	0.276 (2)	0.019 (5)*	
H3	0.685 (2)	0.548 (2)	0.448 (2)	0.027 (5)*	
H6	0.5414 (19)	0.1598 (18)	0.474 (2)	0.020 (5)*	

Atomic displacement parameters (\AA^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
S20	0.0212 (2)	0.0176 (2)	0.0164 (2)	0.00214 (15)	0.00069 (16)	-0.00209 (14)

S20'	0.066 (7)	0.043 (6)	0.032 (5)	0.012 (5)	0.014 (5)	-0.003 (4)
O20	0.0213 (6)	0.0183 (6)	0.0276 (6)	0.0039 (4)	-0.0006 (5)	-0.0006 (4)
C20	0.0207 (8)	0.0428 (11)	0.0277 (9)	0.0050 (7)	0.0044 (7)	0.0087 (8)
C21	0.0272 (9)	0.0267 (9)	0.0331 (10)	0.0027 (7)	0.0064 (7)	0.0094 (7)
C6	0.0245 (8)	0.0151 (7)	0.0226 (8)	-0.0018 (6)	0.0091 (7)	-0.0008 (6)
F9	0.0293 (5)	0.0233 (5)	0.0253 (5)	0.0022 (4)	0.0017 (4)	0.0084 (4)
O7	0.0295 (6)	0.0268 (6)	0.0237 (6)	-0.0024 (5)	-0.0019 (5)	0.0068 (5)
O8	0.0273 (6)	0.0261 (6)	0.0280 (7)	-0.0053 (5)	-0.0048 (5)	0.0013 (5)
N1	0.0190 (7)	0.0211 (7)	0.0173 (7)	-0.0046 (5)	0.0007 (5)	-0.0029 (5)
N3	0.0211 (7)	0.0140 (6)	0.0212 (7)	-0.0032 (5)	0.0029 (5)	-0.0001 (5)
C2	0.0195 (7)	0.0206 (7)	0.0176 (7)	-0.0001 (6)	0.0050 (6)	-0.0008 (6)
C4	0.0194 (7)	0.0199 (7)	0.0190 (7)	-0.0005 (6)	0.0043 (6)	-0.0004 (6)
C5	0.0223 (7)	0.0180 (7)	0.0188 (7)	0.0020 (6)	0.0050 (6)	0.0033 (6)

Geometric parameters (\AA , $^{\circ}$)

S20—O20	1.5288 (12)	C21—H21D	0.96
S20—C21	1.7710 (18)	C21—H21E	0.96
S20—C20	1.7729 (18)	C21—H21F	0.96
S20'—O20	1.492 (7)	C6—C5	1.330 (2)
S20'—C20	1.691 (7)	C6—N1	1.371 (2)
S20'—C21	1.734 (7)	C6—H6	0.94 (2)
C20—H20A	0.96	F9—C5	1.3534 (18)
C20—H20B	0.96	O7—C2	1.2192 (19)
C20—H20C	0.96	O8—C4	1.2215 (19)
C20—H20D	0.96	N1—C2	1.364 (2)
C20—H20E	0.96	N1—H1	0.79 (2)
C20—H20F	0.96	N3—C2	1.377 (2)
C21—H21A	0.96	N3—C4	1.378 (2)
C21—H21B	0.96	N3—H3	0.82 (2)
C21—H21C	0.96	C4—C5	1.446 (2)
O20—S20—C21	106.60 (8)	C2—N1—C6	122.53 (14)
O20—S20—C20	105.89 (8)	C2—N1—H1	114.2 (14)
C21—S20—C20	98.44 (9)	C6—N1—H1	123.3 (14)
O20—S20—H20E	126.7	C2—N3—C4	127.20 (14)
C21—S20—H20E	110.1	C2—N3—H3	116.1 (14)
O20—S20—H21F	126.7	C4—N3—H3	116.6 (14)
C20—S20—H21F	110.9	O7—C2—N1	122.98 (15)
H20E—S20—H21F	104.4	O7—C2—N3	121.84 (15)
O20—S20'—C20	111.9 (5)	N1—C2—N3	115.18 (14)
O20—S20'—C21	110.2 (4)	O8—C4—N3	122.22 (15)
C20—S20'—C21	103.2 (4)	O8—C4—C5	125.40 (15)
S20'—C20—H20C	66.5	N3—C4—C5	112.37 (13)
C5—C6—N1	120.15 (15)	C6—C5—F9	121.11 (14)
C5—C6—H6	123.3 (12)	C6—C5—C4	122.48 (14)
N1—C6—H6	116.6 (12)	F9—C5—C4	116.41 (14)

C5—C6—N1—C2	0.9 (2)	N1—C6—C5—F9	−179.01 (14)
C6—N1—C2—O7	177.16 (15)	N1—C6—C5—C4	0.5 (2)
C6—N1—C2—N3	−2.8 (2)	O8—C4—C5—C6	−178.74 (17)
C4—N3—C2—O7	−176.16 (16)	N3—C4—C5—C6	0.2 (2)
C4—N3—C2—N1	3.8 (2)	O8—C4—C5—F9	0.8 (2)
C2—N3—C4—O8	176.46 (16)	N3—C4—C5—F9	179.76 (13)
C2—N3—C4—C5	−2.5 (2)		

Hydrogen-bond geometry (Å, °)

D—H···A	D—H	H···A	D···A	D—H···A
N1—H1···O20	0.79 (2)	2.04 (2)	2.838 (2)	175 (2)
N3—H3···O20 ⁱ	0.82 (2)	1.97 (2)	2.790 (2)	173 (2)
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